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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: JEFFREY M. FRIEDMAN, YIYING ZHANG, RICARDO PROENCA, MARGHERITA MAFFEI, JEFFREY HALAAS, KETAN GAJIWALA, AND STEPHEN K. BURLEY

(ii) TITLE OF INVENTION: OB POLYPEPTIDE ANTIBODIES AND METHOD OF MAKING (AS AMENDED)

(iii) NUMBER OF SEQUENCES: 102

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Klauber & Jackson
(B) STREET: 411 Hackensack Avenue
(C) CITY: Hackensack
(D) STATE: New Jersey
(E) COUNTRY: USA
(F) ZIP: 07601

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

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(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Jackson Esq., David A.
(B) REGISTRATION NUMBER: 26,742

(C) REFERENCE/DOCKET NUMBER: 600-1-087 CIP 2D

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 201 487-5800

(B) TELEFAX: 201 343-1684

(C) TELEX: 133521

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2793 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) DESCRIPTION: Murine ob cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Murine

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 57..560

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGATCCCTGC TCCAGCAGCT GCAAGGTGCA AGAAGAAGAA GATCCCAGGG AGGAAA	56
ATG TGC TGG AGA CCC CTG TGT CGG TTC CTG TGG CTT TGG TCC TAT CTG	104
Met Cys Trp Arg Pro Leu Cys Arg Phe Leu Trp Leu Trp Ser Tyr Leu	
1 5 10 15	
TCT TAT GTT CAA GCA GTG CCT ATC CAG AAA GTC CAG GAT GAC ACC AAA	152
Ser Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys	
20 25 30	
ACC CTC ATC AAG ACC ATT GTC ACC AGG ATC AAT GAC ATT TCA CAC ACG	200
Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr	
35 40 45	
CAG TCG GTA TCC GCC AAG CAG AGG GTC ACT GGC TTG GAC TTC ATT CCT	248
Gln Ser Val Ser Ala Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro	
50 55 60	
GGG CTT CAC CCC ATT CTG AGT TTG TCC AAG ATG GAC CAG ACT CTG GCA	296
Gly Leu His Pro Ile Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala	
65 70 75 80	
GTC TAT CAA CAG GTC CTC ACC AGC CTG CCT TCC CAA AAT GTG CTG CAG	344
Val Tyr Gln Gln Val Leu Thr Ser Leu Pro Ser Gln Asn Val Leu Gln	
85 90 95	
ATA GCC AAT GAC CTG GAG AAT CTC CGA GAC CTC CTC CAT CTG CTG GCC	392
Ile Ala Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala	
100 105 110	
TTC TCC AAG AGC TGC TCC CTG CCT CAG ACC AGT GGC CTG CAG AAG CCA	440
Phe Ser Lys Ser Cys Ser Leu Pro Gln Thr Ser Gly Leu Gln Lys Pro	
115 120 125	
GAG AGC CTG GAT GGC GTC CTG GAA GCC TCA CTC TAC TCC ACA GAG GTG	488
Glu Ser Leu Asp Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val	
130 135 140	

GTG GCT TTG AGC AGG CTG CAG GGC TCT CTG CAG GAC ATT CTT CAA CAG	536
Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Ile Leu Gln Gln	
145 150 155 160	
TTG GAT GTT AGC CCT GAA TGC TGA AGTTTCAAAG GCCACCAGGC TCCCAAGA	588
Leu Asp Val Ser Pro Glu Cys *	
165	
ATCATGTAGA GGAAGAAAC CTTGGCTTCC AGGGGTCTTC AGGAGAAGAG AGCCATGTGC	648
ACACATCCAT CATTCATTTT TCTCCCTCCT GTAGACCACC CATCCAAAGG CATGACTCCA	708
CAATGCTTGA CTCAAGTTAT CCACACAAC TCATGAGCAC AAGGAGGGGC CAGCCTGCAG	768
AGGGGACTCT CACCTAGTTC TTCAGCAAGT AGAGATAAGA GCCATCCCAT CCCCTCCATG	828
TCCCACCTGC TCCGGGTACA TGTTCTCTCCG TGGGTACACG CTTGCTGCGC GCCCAGGAGA	888
GGTGAGGTAG GGATGGGTAG AGCCTTTGGG CTGTCTCAGA GTCTTTGGGA GCACCGTGAA	948
GGCTGCATCC ACACACAGCT GGAAACTCCC AAGCAGCACA CGATGGAAGC ACTTATTTAT	1008
TTATTCTGCA TTCTATTTTG GATGGATCTG AAGCAAGGCA TCAGCTTTTT CAGGCTTTGG	1068
GGGTCAGCCA GGATGAGGAA GGCTCCTGGG GTGCTGCTTT CAATCCTATT GATGGGTCTG	1128
CCCAGGCAA ACCTAATTTT TGAGTGAAGT GAAGGAAGGT TGGGATCTTC CAAACAAGAG	1188
TCTATGCAGG TAGCGCTCAA GATTGACCTC TGGTGAAGT TTTTGTCTCT ATTGTGACTG	1248
ACTCTATCCA AACACGTTTG CAGCGGCATT GCCGGGAGCA TAGGCTAGGT TATTATCAAA	1308
AGCAGATGAA TTTTGTCAAAG TGAATATGT ATCTATGTGC ACCTGAGGGT AGAGGATGTG	1368
TTAGAGGGAG GGTGAAGGAT CCGGAAGTGT TCTCTGAATT ACATATGTGT GGTAGGCTTT	1428
TCTGAAAGGG TGAGGCATTT TCTTACCTCT GTGGCCACAT AGTGTGGCTT TGTGAAAAGG	1488
ACAAAGGAGT TGAATCTTTC CGGAACATTT GGAGTGATACC AGGCACCCTT GGAGGGGCTA	1548
AAGCTACAGG CCTTTTGTG GATATTTGCT GAGCTCAGGG AGTGAGGGCC CCACATTTGA	1608
GACAGTGAGC CCCAAGAAAA GGGTCCCTGG TGTAGATCTC CAAGGTTGTC CAGGGTTGAT	1668
CTCACAATGC GTTCTTTAAG CAGGTAGACG TTTGCATGCC AATATGTGGT TCTCATCTGA	1728
TTGGTTTCATC CAAAGTAGAA CCCTGTCTCC CACCCATTCT GTGGGGAGTT TTGTTCCAGT	1788
GGGAATGAGA AATCACTTAG CAGATGGTCC TGAGCCCTGG GCCAGCACTG CTGAGGAAGT	1848
GCCAGGGCCC CAGGCCAGGC TGCCAGAATT GCCCTTCGGG CTGGAGGATG AACAAAGGGG	1908
CTTGGGTTTT TCCATCACCC CTGCACCCTA TGTCACCATC AAATGGGGG GCAGATCAGT	1968
GAGAGGACAC TTGATGGAAA GCAATACACT TTAAGACTGA GCACAGTTTC GTGCTCAGCT	2028
CTGTCTGGTG CTGTGAGCTA GAGAAGCTCA CCACATACAT ATAAAAATCA GAGGCTCATG	2088
TCCCTGTGGT TAGACCCCTAC TCGCGGCGGT GACTTCCACC ACAGCAGCAC CGCACCCTG	2148
GAAGTACAGT GCTGTCTTCA ACAGGTGTGA AAGAACCTGA GCTGAGGGTG ACAGTGCCCA	2208
GGGGAACCTT GCTTGCAGTC TATTGCATTT ACATACCGCA TTTCAGGGCA CATTAGCATC	2268
CACTCCTATG GTAGCACACT GTTGACAATA GGACAAGGGA TAGGGGTTGA CTATCCCTTA	2328
TCCAAAATGC TTGGGACTAG AAGAGTTTTG GATTTTAGAG TCTTTTCAGG CATAGGTATA	2388
TTTGAGTATA TATAAAATGA GATATCTTGG GGATGGGGCC CAAGTATAAA CATGAAGTTC	2448

ATTTATATTT CATAATACCG TATAGACACT GCTTGAAGTG TAGTTTTATA CAGTGTTTTA 2508
 AATAACGTTG TATGCATGAA AGACGTTTTT ACAGCATGAA CCTGTCTACT CATGCCAGCA 2568
 CTCAAAAACC TTGGGGTTTT GGAGCAGTTT GGATCTTGGG TTTTCTGTTA AGAGATGGTT 2628
 AGCTTATACC TAAAACCATA ATGGCAAACA GGCTGCAGGA CCAGACTGGA TCCTCAGCCC 2688
 TGAAGTGTGC CCTTCCAGCC AGGTCATACC CTGTGGAGGT GAGCGGGATC AGGTTTTGTG 2748
 GTGCTAAGAG AGGAGTTGGA GGTAGATTTT GGAGGATCTG AGGGC 2793

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (A) DESCRIPTION: Murine ob polypeptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Cys	Trp	Arg	Pro	Leu	Cys	Arg	Phe	Leu	Trp	Leu	Trp	Ser	Tyr	Leu	1	5	10	15
Ser	Tyr	Val	Gln	Ala	Val	Pro	Ile	Gln	Lys	Val	Gln	Asp	Asp	Thr	Lys	20	25	30	
Thr	Leu	Ile	Lys	Thr	Ile	Val	Thr	Arg	Ile	Asn	Asp	Ile	Ser	His	Thr	35	40	45	
Gln	Ser	Val	Ser	Ala	Lys	Gln	Arg	Val	Thr	Gly	Leu	Asp	Phe	Ile	Pro	50	55	60	
Gly	Leu	His	Pro	Ile	Leu	Ser	Leu	Ser	Lys	Met	Asp	Gln	Thr	Leu	Ala	65	70	75	80
Val	Tyr	Gln	Gln	Val	Leu	Thr	Ser	Leu	Pro	Ser	Gln	Asn	Val	Leu	Gln	85	90	95	
Ile	Ala	Asn	Asp	Leu	Glu	Asn	Leu	Arg	Asp	Leu	Leu	His	Leu	Leu	Ala	100	105	110	
Phe	Ser	Lys	Ser	Cys	Ser	Leu	Pro	Gln	Thr	Ser	Gly	Leu	Gln	Lys	Pro	115	120	125	
Glu	Ser	Leu	Asp	Gly	Val	Leu	Glu	Ala	Ser	Leu	Tyr	Ser	Thr	Glu	Val	130	135	140	
Val	Ala	Leu	Ser	Arg	Leu	Gln	Gly	Ser	Leu	Gln	Asp	Ile	Leu	Gln	Gln	145	150	155	160
Leu	Asp	Val	Ser	Pro	Glu	Cys										165			

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 700 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(A) DESCRIPTION: Human ob cDNA where N represents any nucleotide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 46..546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

NNNGNNGTTG CAAGGCCCAA GAAGCCCAANN NTCCTGGGAA GGAAA ATG CAT TGG	54
Met His Trp	
1	
GGA ACC CTG TGC GGA TTC TTG TGG CTT TGG CCC TAT CTT TTC TAT GTC	102
Gly Thr Leu Cys Gly Phe Leu Trp Leu Trp Pro Tyr Leu Phe Tyr Val	
5 10 15	
CAA GCT GTG CCC ATC CAA AAA GTC CAA GAT GAC ACC AAA ACC CTC ATC	150
Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile	
20 25 30 35	
AAG ACA ATT GTC ACC AGG ATC AAT GAC ATT TCA CAC ACG CAG TCA GTC	198
Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val	
40 45 50	
TCC TCC AAA CAG AAA GTC ACC GGT TTG GAC TTC ATT CCT GGG CTC CAC	246
Ser Ser Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His	
55 60 65	
CCC ATC CTG ACC TTA TCC AAG ATG GAC CAG ACA CTG GCA GTC TAC CAA	294
Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln	
70 75 80	
CAG ATC CTC ACC AGT ATG CCT TCC AGA AAC GTG ATC CAA ATA TCC AAC	342
Gln Ile Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln Ile Ser Asn	
85 90 95	
GAC CTG GAG AAC CTC CGG GAT CTT CTT CAC GTG CTG GCC TTC TCT AAG	390
Asp Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala Phe Ser Lys	
100 105 110 115	
AGC TGC CAC TTG CCC TGG GCC AGT GGC CTG GAG ACC TTG GAC AGC CTG	438
Ser Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu Asp Ser Leu	
120 125 130	
GGG GGT GTC CTG GAA GCT TCA GGC TAC TCC ACA GAG GTG GTG GCC CTG	486
Gly Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val Val Ala Leu	
135 140 145	
AGC AGG CTG CAG GGG TCT CTG CAG GAC ATG CTG TGG CAG CTG GAC CTC	534
Ser Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln Leu Asp Leu	
150 155 160	
AGC CCT GGG TGC TGAGGCCTT GAAGGTCACCT CTCCTGCAA GGACTNACGT	585
Ser Pro Gly Cys	
165	
TAAGGGAAGG AACTCTGGTT TCCAGGTATC TCCAGGATTG AAGAGCATTG CATGGACACC	645
CCTTATCCAG GACTCTGTCA ATTTCCCTGA CTCCTCTAAG CCACTCTTCC AAAGG	700

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (A) DESCRIPTION: Human ob polypeptide

(vi) ORIGINAL SOURCE: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met His Trp Gly Thr Leu Cys Gly Phe Leu Trp Leu Trp Pro Tyr Leu
1 5 10 15
Phe Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys
20 25 30
Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr
35 40 45
Gln Ser Val Ser Ser Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro
50 55 60
Gly Leu His Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala
65 70 75 80
Val Tyr Gln Gln Ile Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln
85 90 95
Ile Ser Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala
100 105 110
Phe Ser Lys Ser Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu
115 120 125
Asp Ser Leu Gly Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val
130 135 140
Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln
145 150 155 160
Leu Asp Leu Ser Pro Gly Cys
165

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (A) DESCRIPTION: Murine ob polypeptide lacking Gln at position

49

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Murine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Cys Trp Arg Pro Leu Cys Arg Phe Leu Trp Leu Trp Ser Tyr Leu
1 5 10 15

Ser Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys
 20 25 30
 Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr
 35 40 45
 Ser Val Ser Ala Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly
 50 55 60
 Leu His Pro Ile Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala Val
 65 70 75 80
 Tyr Gln Gln Val Leu Thr Ser Leu Pro Ser Gln Asn Val Leu Gln Ile
 85 90 95
 Ala Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala Phe
 100 105 110
 Ser Lys Ser Cys Ser Leu Pro Gln Thr Ser Gly Leu Gln Lys Pro Glu
 115 120 125
 Ser Leu Asp Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val Val
 130 135 140
 Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Ile Leu Gln Gln Leu
 145 150 155 160
 Asp Val Ser Pro Glu Cys
 165

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (A) Description: Human ob polypeptide lacking Gln at position

49

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met His Trp Gly Thr Leu Cys Gly Phe Leu Trp Leu Trp Pro Tyr Leu
 1 5 10 15
 Phe Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys
 20 25 30
 Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr
 35 40 45
 Ser Val Ser Ser Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro Gly
 50 55 60
 Leu His Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val
 65 70 75 80
 Tyr Gln Gln Ile Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln Ile
 85 90 95
 Ser Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala Phe
 100 105 110
 Ser Lys Ser Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu Asp

115	120	125
Ser Leu Gly Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val Val		
130	135	140
Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln Leu		
145	150	155
Asp Leu Ser Pro Gly Cys		
165		

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 176 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
 - (A) DESCRIPTION: exon 2G7
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GTGCAAGAAG AAGAAGATCC CAGGGCAGGA AAATGTGCTG GAGACCCCTG TGTCGGGTCC	60
NGTGGNTTTG GTCCTATCTG TCTTATGTNC AAGCAGTGCC TATCCAGAAA GTCCAGGATG	120
ACACCAAAAG CCTCATCAAG ACCATTGTCA NCAGGATCAC TGANATTTC A CACACG	176

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
 - (A) DESCRIPTION: PCR 5' primer for exon 2G7
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CCAGGGCAGG AAAATGTG	18
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(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
 - (A) DESCRIPTION: PCR 3' primer for exon 2G7
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: YES

CATCCTGGAC TTTCTGGATA GG

22

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: peptide

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Cys Trp Arg Pro Leu Cys Arg Phe Leu Trp Leu Trp Ser Tyr Leu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (plasmid)

- (A) DESCRIPTION: pET-15b expression vector

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (ix) FEATURE:

- (A) NAME/KEY: T7 promoter
(B) LOCATION: 20..37

- (ix) FEATURE:

- (A) NAME/KEY: lac operator
(B) LOCATION: 39..64

- (ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 108..243

- (ix) FEATURE:

- (A) NAME/KEY: His-Tag
(B) LOCATION: 123..137

- (ix) FEATURE:

- ```
(A) NAME/KEY: Thrombin cleavage site
(B) LOCATION: 184..196
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGATCTCGAT CCCGCGAAAT TAATACGACT CACTATAGGG GAATTGTGAG CGGATAACAA

60

TTCCCCTCTA CAAATAATTT TGTTTAACTT TAAGAAGGAG ATATACC ATG GGC AGC  
Met Gly Ser

116

AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG CGC GGC AGC 164  
 Ser His His His His His His Ser Ser Gly Leu Val Pro Arg Gly Ser  
           5                                  10                                  15

CAT ATG CTC GAG GAT CCC GCT GCT AAC AAA GCC CGA AAG GAA GCT GAG 212  
 His Met Leu Glu Asp Pro Ala Ala Asn Lys Ala Arg Lys Glu Ala Glu  
           20                                  25                                  30                                  35

TTG GCT GCT GCC ACC GCT GAG CAA TAA CTA G CATAACCCCT TGGGGCCTCT 263  
 Leu Ala Ala Ala Thr Ala Glu Gln \*  
                                   40

AAACGGGTCT TGAGGGGTTT TTTG 287

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro  
   1                                  5                                  10                                  15

Arg Gly Ser His Met Leu Glu Asp Pro Ala Ala Asn Lys Ala Arg Lys  
           20                                  25                                  30

Glu Ala Glu Leu Ala Ala Ala Thr Ala Glu Gln  
           35                                  40

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (primer)

- (A) DESCRIPTION: Murine 5' primer

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CTTATGTTCA TATGGTGCCG ATCCAGAAAG TC

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: Murine 3' primer

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: Yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TCCCTCTACA TATGTCTTGG GAGCCTGGTG GC

32

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: Human 5' primer

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TCTATGTCCA TATGGTGCCG ATCCAAAAAG TC

32

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: Human 3' primer

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: Yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TTCCTTCCCA TATGGTACTC CTTGCAGGAA GA

32

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(A) DESCRIPTION: Splice acceptor site in ob

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: Splice acceptor site

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AGCAGTCGGT A

11

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(A) DESCRIPTION: ob peptide fragment

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Murine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Pro | Ile | Gln | Lys | Val | Gln | Asp | Asp | Thr | Lys | Thr | Leu | Ile | Lys | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(A) DESCRIPTION: ob peptide fragment

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Murine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | His | Pro | Ile | Leu | Ser | Leu | Ser | Lys | Met | Asp | Gln | Thr | Leu | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(A) DESCRIPTION: ob peptide fragment

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Murine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ser Lys Ser Cys Ser Leu Pro Gln Thr Ser Gly Leu Gln Lys Pro Glu  
1 5 10 15

Ser Leu Asp

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

- (A) DESCRIPTION: ob peptide fragment

(v) FRAGMENT TYPE: Carboxyl terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Murine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Ser Arg Leu Gln Gly Ser Leu Gln Asp Ile Leu Gln Gln Leu Asp Val  
1 5 10 15

Ser Pro Glu Cys

## (2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 414 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
  - (A) DESCRIPTION: portion of the human ob gene including noncoding sequence upstream of first exon, coding sequence of first exon, and 5' region of first intron
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Human
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 38..181
- (ix) FEATURE:
  - (A) NAME/KEY: 5' region of first intron
  - (B) LOCATION: 182..414
- (ix) FEATURE:
  - (A) NAME/KEY: 5' noncoding sequence of the human ob gene from which the HOB 1gF DNA primer was generated
  - (B) LOCATION: 11..28
- (ix) FEATURE:
  - (A) NAME/KEY: intronic sequence of the human ob gene from which the HOB 1gR primer was generated
  - (B) LOCATION: 241..260

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```

GGTTGCAAGG CCCAAGAAGC CCATCCTGGG AAGGAAA ATG CAT TGG GGA ACC CTG 55
 Met His Trp Gly Thr Leu
 1 5

TGC GGA TTC TTG TGG CTT TGG CCC TAT CTT TTC TAT GTC CAA GCT GTG 103
Cys Gly Phe Leu Trp Leu Trp Pro Tyr Leu Phe Tyr Val Gln Ala Val
 10 15 20

CCC ATC CAA AAA GTC CAA GAT GAC ACC AAA ACC CTC ATC AAG ACA ATT 151
Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys Thr Ile
 25 30 35

GTC ACC AGG ATC AAT GAC ATT TCA CAC ACG GTAAGGAGAG TATGCGGGGA 201
Val Thr Arg Ile Asn Asp Ile Ser His Thr
 40 45

CAAAGTAGAA CTGCAGCCAG CCCAGCACTG GCTCCTAGTG GCACTGGACC CAGATAGTCC 261

AAGAAACATT TATTGAACGC CTCCTGAATG CCAGGCACCT ACTGGAAGCT GAGAAGGATT 321

TTGGATAGCA CAGGGCTCCA CTCTTTCTGG TTGTTTCTTN TGGCCCCCTC TGCCTGCTGA 381

GATNCCAGGG GTTAGNGGTT CTTAATTCCT AAA 414

```

## (2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(A) DESCRIPTION: N-terminal portion of the human ob protein encoded by first exon

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

```
Met His Trp Gly Thr Leu Cys Gly Phe Leu Trp Leu Trp Pro Tyr Leu
 1 5 10 15
Phe Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys
 20 25 30
Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr
 35 40 45
```

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) DESCRIPTION: portion of the human ob gene including 3' region of first intron, coding sequence of second exon, and 3' noncoding sequence

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 291..648

(ix) FEATURE:

- (A) NAME/KEY: 3' of first intron
- (B) LOCATION: 1..290

(ix) FEATURE:

(A) NAME/KEY: intronic sequence of the human ob gene HOB from which the HOB 2gF primer was generated

(B) LOCATION: 250..269

(ix) FEATURE:

(A) NAME/KEY: 3' noncoding sequence of the human ob gene from which the HOB 2gR DNA primer was generated

(B) LOCATION: 707..728

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```
CTGGTTCTTT CAGGAAGAGG CCATGTAAGA GAAAGGAATT GACCTAGGGA AAATTGGCCT 60
GGGAAGTGGA GGGAACGGAT GGTGTGGGAA AAGCAGGAAT CTCGAGACC AGCTTAGAGG 120
CTTGGCAGTC ACCTGGGTGC AGGANACAAG GGCCTGAGCC AAAGTGGTGA GGGAGGGTGG 180
AAGGAGACAG CCCAGAGAAT GACCCTCCAT GCCCACGGGG AAGGCAGAGG GCTCTGAGAG 240
```



|                                                                   |     |
|-------------------------------------------------------------------|-----|
| CGATTCTCC CACATGCTGA GCACTTGTTT TCCCTCTTCC TCCTNCATAG CAG TCA     | 296 |
| Gln Ser<br>1                                                      |     |
| GTC TCC TCC AAA CAG AAA GTC ACC GGT TTG GAC TTC ATT CCT GGG CTC   | 344 |
| Val Ser Ser Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro Gly Leu   |     |
| 5 10 15                                                           |     |
| CAC CCC ATC CTG ACC TTA TCC AAG ATG GAC CAG ACA CTG GCA GTC TAC   | 392 |
| His Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr   |     |
| 20 25 30                                                          |     |
| CAA CAG ATC CTC ACC AGT ATG CCT TCC AGA AAC GTG ATC CAA ATA TCC   | 440 |
| Gln Gln Ile Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln Ile Ser   |     |
| 35 40 45 50                                                       |     |
| AAC GAC CTG GAG AAC CTC CGG GAT CTT CTT CAC GTG CTG GCC TTC TCT   | 488 |
| Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala Phe Ser   |     |
| 55 60 65                                                          |     |
| AAG AGC TGC CAC TTG CCC TGG GCC AGT GGC CTG GAG ACC TTG GAC AGC   | 536 |
| Lys Ser Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu Asp Ser   |     |
| 70 75 80                                                          |     |
| CTG GGG GGT GTC CTG GAA GCT TCA GGC TAC TCC ACA GAG GTG GTG GCC   | 584 |
| Leu Gly Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val Val Ala   |     |
| 85 90 95                                                          |     |
| CTG AGC AGG CTG CAG GGG TCT CTG CAG GAC ATG CTG TGG CAG CTG GAC   | 632 |
| Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln Leu Asp   |     |
| 100 105 110                                                       |     |
| CTC AGC CCT GGG TGC T GAGGCCTTGA AGGTCACTCT TCCTGCAAGG ACTACGTTAA | 688 |
| Leu Ser Pro Gly Cys                                               |     |
| 115                                                               |     |
| GGGAAGGAAC TCTGGCTTTC CAGGTATCTC CAGGATTGAA GAGCATTGCA TGGACACCCC | 748 |
| TTATCCAGGA CTCTGTCAAT TTCCCTGACT CCTCTAAGCC ACTCTTCCAA AGG        | 801 |

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(A) DESCRIPTION: C-terminal portion of the human ob protein encoded by second exon

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Gln Ser Val Ser Ser Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro |  |
| 1 5 10 15                                                       |  |
| Gly Leu His Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala |  |
| 20 25 30                                                        |  |
| Val Tyr Gln Gln Ile Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln |  |
| 35 40 45                                                        |  |
| Ile Ser Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala |  |
| 50 55 60                                                        |  |
| Phe Ser Lys Ser Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu |  |
| 65 70 75 80                                                     |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Ser | Leu | Gly | Gly | Val | Leu | Glu | Ala | Ser | Gly | Tyr | Ser | Thr | Glu | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Ala | Leu | Ser | Arg | Leu | Gln | Gly | Ser | Leu | Gln | Asp | Met | Leu | Trp | Gln |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Asp | Leu | Ser | Pro | Gly | Cys |     |     |     |     |     |     |     |     |     |
|     |     | 115 |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: pichia yeast
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Leu Glu Lys Arg Glu Ala Glu Ala  
 1 5

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: pichia yeast
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Glu Ala Glu Ala  
 1

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (v) FRAGMENT TYPE: Internal
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: pichia yeast
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Leu Glu Lys Arg  
 1

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
  - (A) DESCRIPTION: HOB IgF DNA primer generated from the 5' noncoding sequence of the human ob gene
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CCCAAGAAGC CCATCCTG

18

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
  - (A) DESCRIPTION: HOB IgR DNA primer generated from the first intronic sequence of the human ob gene
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GACTATCTGG GTCCAGTGCC

20

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
  - (A) DESCRIPTION: HOB 2gF DNA primer generated from the first intronic sequence of the human ob gene
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CCACATGCTG AGCACTTGTT

20

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: HOB 2gR DNA primer generated from the 3' noncoding sequence of the human ob gene

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTTCAATCCT GGAGATACCT GG

22

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA

(A) DESCRIPTION: pPIC.9 cloning site

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CTCGAGAAAA GAGAGGCTGA AGCTTACGTA GAATTCCTA GGCCGGCCGG G

51

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: PCR 5' primer for amplifying human ob cDNA sequence

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GTATCTCTCG AGAAAAGAGT GCCCATCCAA AAAGTCCAAG

40

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: PCR 3' primer for amplifying human ob cDNA sequence

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GCGCGAATTC TCAGCACCCA GGGCTGAGGT C

31

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: PCR 5' primer for amplifying murine ob cDNA sequence

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GTATCTCTCG AGAAAAGAGT GCCTATCCAG AAAGTCCAGG

40

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: PCR 3' primer for amplifying murine ob cDNA sequence

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GCGCGAATTC TCAGCATTCA GGGCTAACAT C

31

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(A) DESCRIPTION: tetrapeptide at N-terminus of renatured murine ob protein after thrombin cleavage

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Murine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Gly Ser His Met

1

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer sWSS1734

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CAAGACAAAT GAGATAAGG

19

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer sWSS1734

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

AGAGTTACAG CTTTACAG

18

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer sWSS494

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CTAAACACCT TTCCATTCC

19

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer swSS494

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

TTATATTAC TTTCCCTC TC

22

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer swSS883

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

TGCAGTAAGC TGTGATTGAG

20

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer swSS883

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GTGCAGCTTT AATTGTGAGC

20

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (primer)
  - (A) DESCRIPTION: sequence tagged-site specific PCR primer sWSS2359

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

AGTGTTGTGT TTCTCCTG

18

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (primer)
  - (A) DESCRIPTION: sequence tagged-site specific PCR primer sWSS2359

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

AAAGGGGATG TGATAAGTG

19

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (primer)
  - (A) DESCRIPTION: sequence tagged-site specific PCR primer sWSS2336

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GGTGTTACGT TTAGTTAC

18



(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
  - (A) DESCRIPTION: sequence tagged-site specific PCR primer sWSS2336
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Human
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GGAATAATGA GAGAAGATTG

20

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
  - (A) DESCRIPTION: sequence tagged-site specific PCR primer sWSS1218
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Human
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GCTCAACTGA CAGAAAAC

18

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
  - (A) DESCRIPTION: sequence tagged-site specific PCR primer sWSS1218
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Human
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GACTATGTAA AAGAAATGCC

20

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
  - (A) DESCRIPTION: sequence tagged-site specific PCR primer sWSS1402
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Human
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

AAAGGGCTTC TAATCTAC

18

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
  - (A) DESCRIPTION: sequence tagged-site specific PCR primer sWSS1402
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Human
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CCTTCCAAC TCTTTGAC

18

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
  - (A) DESCRIPTION: sequence tagged-site specific PCR primer sWSS999
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Human
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TAAACCCCTT TCTGTTC

18

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer swSS999

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

TTGCATAATA GTCACACCC

19

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer swSS1751

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CCAAAATCAG AATTGTCAGA AG

22

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer swSS1751

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

AAACCGAAGT TCAGATACAG

20

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
  - (A) DESCRIPTION: sequence tagged-site specific PCR primer sWSS1174
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Human
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

AATATCTGAC ATTGGCAC

18

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
  - (A) DESCRIPTION: sequence tagged-site specific PCR primer sWSS1174
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Human
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

TTAGACCTGA GAAAAGAG

18

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
  - (A) DESCRIPTION: sequence tagged-site specific PCR primer sWSS2061
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Human
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GTTGCACAAT ACAAATCC

19

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
  - (A) DESCRIPTION: sequence tagged-site specific PCR primer sWSS2061
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Human
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CTTCCATTAG TGTCTTATAG

20

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
  - (A) DESCRIPTION: sequence tagged-site specific PCR primer sWSS2588
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Human
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

ATCACTACAC ACCTAATC

18

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
  - (A) DESCRIPTION: sequence tagged-site specific PCR primer sWSS2588
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Human
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CCATTCTACA TTTCCACC

18

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
  - (A) DESCRIPTION: sequence tagged-site specific PCR primer swSS808
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Human
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GGCTGTGTGA GCAAGATCCT AGGA

24

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
  - (A) DESCRIPTION: sequence tagged-site specific PCR primer swSS808
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Human
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

TTGCCAGGCA AAGAGGGCTG GAC

23

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
  - (A) DESCRIPTION: sequence tagged-site specific PCR primer swSS1392
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Human
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

CTCAGGTATG TCTTTATC

18

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer sWSS1392

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

TGTCTCTGCA TTCTTTTC

18

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer sWSS1148

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GACACATACA AACACAAG

18

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer sWSS1148

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

ATTGAGTTGA GTGTAGTAG

19

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)  
(A) DESCRIPTION: sequence tagged-site specific PCR primer sWSS1529

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CAGGGATTTC TAATTGTC

18

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)  
(A) DESCRIPTION: sequence tagged-site specific PCR primer sWSS1529

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

AAAAGATGGA GGCTTTTG

18

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)  
(A) DESCRIPTION: sequence tagged-site specific PCR primer sWSS2619

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CGTTAAGGGA AGGAACTCTG G

21

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single



(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer swSS2619

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TGGCTTAGAG GAGTCAGGGA

20

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer swSS404

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

ACCAGGGTCA ATACAAAG

18

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer swSS404

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

TAATGTGTCC TTCTTGCC

18

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (primer)
  - (A) DESCRIPTION: sequence tagged-site specific PCR primer swSS2367
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Human
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CAATCCTGGC TTCATTG

18

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
  - (A) DESCRIPTION: sequence tagged-site specific PCR primer swSS2367
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Human
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

AAGGTGGGTA GGATGCTA

18

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
  - (A) DESCRIPTION: Marker UT528
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Human
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

TGCAGTAAGC TGTGATTGAG

20

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)  
(A) DESCRIPTION: Marker UT528

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

GTGCAGCTTT AATTGTGAGC

20

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)  
(A) DESCRIPTION: Marker AFMa065zg9

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

AGCTTCAAGA CTTTNAGCCT

20

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)  
(A) DESCRIPTION: Marker AFMa065zg9

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GGTCAGCAGC ACTGTGATT

19

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)  
(A) DESCRIPTION: Marker AFMa125wh1

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TCACCTTGAG ATTCCATCC

19

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)  
(A) DESCRIPTION: Marker AFMa125wh1

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

AACACCGTGG TCTTATCAA

20

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)  
(A) DESCRIPTION: Marker AFM309yf10

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

CATCCAAGTT GGCAGTTTTT

20

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)  
(A) DESCRIPTION: Marker AFM309yf10

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

AGATGCTGAA TTCCCAGACA

20

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)  
(A) DESCRIPTION: Marker AFM218xf10

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

TGGGCAACAC AGCAAA

16

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)  
(A) DESCRIPTION: Marker AFM218xf10

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

TGCAGTTAGT GCCAATGTCA

20

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)  
(A) DESCRIPTION: Marker AFM206xc1

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Human
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

CCAGGCCATG TGGAAC

16

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
  - (A) DESCRIPTION: Marker AFM206xc1
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Human
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

AGTTCTTGGC TTGCGTCAGT

20

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
  - (A) DESCRIPTION: Marker AFM199xh12
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Human
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

TCTGATTGCT GGCTGC

16

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
  - (A) DESCRIPTION: Marker AFM199xh12

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Human
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GCGCGTGTGT ATGTGAG

17

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
  - (A) DESCRIPTION: Marker AFMa345wc9
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Human
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

AGCTCTTGGC AAATCACAT

20

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
  - (A) DESCRIPTION: Marker AFMa345wc9
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Human
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

GCCTAAGGGA ATGAGACACA

20

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
  - (A) DESCRIPTION: primer for mouse Pax4 gene
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: murine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GGGAGCCTTG TCCTGGGTAC AAAG

24

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 491 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA  
 (A) DESCRIPTION: Recombinant murine met ob

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: murine

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 41..478

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

|                                                                 |     |     |     |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|-----|-----|-----|
| TCTAGATTTG AGTTTAACT TTTAGAAGGA GGAATAACAT                      | ATG | GTA | CCG | ATC | CAG | 55  |
|                                                                 | Met | Val | Pro | Ile | Gln |     |
|                                                                 | 1   |     |     |     | 5   |     |
| AAA GTT CAG GAC GAC ACC AAA ACC TTA ATT AAA ACG ATC GTT ACG CGT |     |     |     |     |     | 103 |
| Lys Val Gln Asp Thr Lys Thr Leu Ile Lys Thr Ile Val Thr Arg     |     |     |     |     |     |     |
|                                                                 | 10  |     | 15  |     | 20  |     |
| ATC AAC GAC ATC AGT CAC ACC CAG TCG GTC TCC GCT AAA CAG CGT GTT |     |     |     |     |     | 151 |
| Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser Ala Lys Gln Arg Val |     |     |     |     |     |     |
|                                                                 | 25  |     | 30  |     | 35  |     |
| ACC GGT CTG GAC TTC ATC CCG GGT CTG CAC CCG ATC CTA AGC TTG TCC |     |     |     |     |     | 199 |
| Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro Ile Leu Ser Leu Ser |     |     |     |     |     |     |
|                                                                 | 40  |     | 45  |     | 50  |     |
| AAA ATG GAC CAG ACC CTG GCT GTA TAC CAG CAG GTG TTA ACC TCC CTG |     |     |     |     |     | 247 |
| Lys Met Asp Gln Thr Leu Ala Val Tyr Gln Gln Val Leu Thr Ser Leu |     |     |     |     |     |     |
|                                                                 | 55  |     | 60  |     | 65  |     |
| CCG TCC CAG AAC GTT CTT CAG ATC GCT AAC GAC CTC GAG AAC CTT CGC |     |     |     |     |     | 295 |
| Pro Ser Gln Asn Val Leu Gln Ile Ala Asn Asp Leu Glu Asn Leu Arg |     |     |     |     |     |     |
|                                                                 | 70  |     | 75  |     | 80  | 85  |
| GAC CTG CTG CAC CTG CTG GCA TTC TCC AAA TCC TGC TCC CTG CCG CAG |     |     |     |     |     | 343 |
| Asp Leu Leu His Leu Leu Ala Phe Ser Lys Ser Cys Ser Leu Pro Gln |     |     |     |     |     |     |
|                                                                 | 90  |     | 95  |     | 100 |     |
| ACC TCA GGT CTT CAG AAA CCG GAA TCC CTG GAC GGG GTC CTG GAA GCA |     |     |     |     |     | 391 |
| Thr Ser Gly Leu Gln Lys Pro Glu Ser Leu Asp Gly Val Leu Glu Ala |     |     |     |     |     |     |
|                                                                 | 105 |     | 110 |     | 115 |     |



|                                                                 |     |
|-----------------------------------------------------------------|-----|
| TCC CTG TAC AGC ACC GAA GTT GTT GCT CTG TCC CGT CTG CAG GGT TCC | 439 |
| Ser Leu Tyr Ser Thr Glu Val Val Ala Leu Ser Arg Leu Gln Gly Ser |     |
| 120 125 130                                                     |     |
|                                                                 |     |
| CTT CAG GAC ATC CTT CAG CAG CTG GAC GTT TCT CCG GAA TGT TAATGGA | 488 |
| Leu Gln Asp Ile Leu Gln Gln Leu Asp Val Ser Pro Glu Cys         |     |
| 135 140 145                                                     |     |
|                                                                 |     |
| TCC                                                             | 491 |

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (A) DESCRIPTION: Recombinant murine met ob protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys |  |
| 1 5 10 15                                                       |  |
|                                                                 |  |
| Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser |  |
| 20 25 30                                                        |  |
|                                                                 |  |
| Ala Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro |  |
| 35 40 45                                                        |  |
|                                                                 |  |
| Ile Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln Gln |  |
| 50 55 60                                                        |  |
|                                                                 |  |
| Val Leu Thr Ser Leu Pro Ser Gln Asn Val Leu Gln Ile Ala Asn Asp |  |
| 65 70 75 80                                                     |  |
|                                                                 |  |
| Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala Phe Ser Lys Ser |  |
| 85 90 95                                                        |  |
|                                                                 |  |
| Cys Ser Leu Pro Gln Thr Ser Gly Leu Gln Lys Pro Glu Ser Leu Asp |  |
| 100 105 110                                                     |  |
|                                                                 |  |
| Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val Val Ala Leu Ser |  |
| 115 120 125                                                     |  |
|                                                                 |  |
| Arg Leu Gln Gly Ser Leu Gln Asp Ile Leu Gln Gln Leu Asp Val Ser |  |
| 130 135 140                                                     |  |
|                                                                 |  |
| Pro Glu Cys                                                     |  |
| 145                                                             |  |

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (A) DESCRIPTION: Recombinant human met ob

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: human

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 4..444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| CAT ATG GTA CCG ATC CAG AAA GTT CAG GAC GAC ACC AAA ACC TTA ATT | 48  |
| Met Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile     |     |
| 1 5 10 15                                                       |     |
| AAA ACG ATC GTT ACG CGT ATC AAC GAC ATC AGT CAC ACC CAG TCG GTG | 96  |
| Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val |     |
| 20 25 30                                                        |     |
| AGC TCT AAA CAG CGT GTT ACA GGC CTG GAC TTC ATC CCG GGT CTG CAC | 144 |
| Ser Ser Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His |     |
| 35 40 45                                                        |     |
| CCG ATC CTG ACC TTG TCC AAA ATG GAC CAG ACC CTG GCT GTA TAC CAG | 192 |
| Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln |     |
| 50 55 60                                                        |     |
| CAG ATC TTA ACC TCC ATG CCG TCC CGT AAC GTT CTT CAG ATC TCT AAC | 240 |
| Gln Ile Leu Thr Ser Met Pro Ser Arg Asn Val Leu Gln Ile Ser Asn |     |
| 65 70 75                                                        |     |
| GAC CTC GAG AAC CTT CGC GAC CTG CTG CAC GTG CTG GCA TTC TCC AAA | 288 |
| Asp Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala Phe Ser Lys |     |
| 80 85 90 95                                                     |     |
| TCC TGC CAC CTG CCA TGG GCT TCA GGT CTT GAG ACT CTG GAC TCT CTG | 336 |
| Ser Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu Asp Ser Leu |     |
| 100 105 110                                                     |     |
| GGC GGG GTC CTG GAA GCA TCC GGT TAC AGC ACC GAA GTT GTT GCT CTG | 384 |
| Gly Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val Val Ala Leu |     |
| 115 120 125                                                     |     |
| TCC CGT CTG CAG GGT TCC CTT CAG GAC ATG CTT TGG CAG CTG GAC CTG | 432 |
| Ser Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln Leu Asp Leu |     |
| 130 135 140                                                     |     |
| TCT CCG GGT TGT TAATGGATCC                                      | 454 |
| Ser Pro Gly Cys                                                 |     |
| 145                                                             |     |

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 147 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein  
 (A) DESCRIPTION: Recombinant human met ob protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

|                                                                 |
|-----------------------------------------------------------------|
| Met Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys |
| 1 5 10 15                                                       |
| Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser |
| 20 25 30                                                        |

Ser Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro  
           35                          40                          45  
 Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln Gln  
           50                          55                          60  
 Ile Leu Thr Ser Met Pro Ser Arg Asn Val Leu Gln Ile Ser Asn Asp  
           65                          70                          75                          80  
 Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala Phe Ser Lys Ser  
                           85                          90                          95  
 Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu Asp Ser Leu Gly  
                           100                          105                          110  
 Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val Val Ala Leu Ser  
           115                          120                          125  
 Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln Leu Asp Leu Ser  
           130                          135                          140  
 Pro Gly Cys  
 145

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:  
     (A) LENGTH: 21 amino acids  
     (B) TYPE: amino acid  
     (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro  
   1                          5                          10                          15  
 Arg Gly Ser His Met  
                           20

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:  
     (A) LENGTH: 7 amino acids  
     (B) TYPE: amino acid  
     (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Glu Asn Leu Arg Asp Leu Leu  
   1                          5

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:  
     (A) LENGTH: 21 base pairs  
     (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA  
(A) DESCRIPTION: wild-type (normal) sequence in region of nonsense mutation in ob/ob (1J) mice

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:  
GAGAATCTCC GAGACCTCCT C

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 3 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: C-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Glu Asn Leu  
1

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA  
(A) DESCRIPTION: mutant sequence in region of nonsense mutation in ob/ob (1J) mice leading to premature stop codon

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:  
GAGAATCTCT GAGACCTCCT C